

Fig. 1A

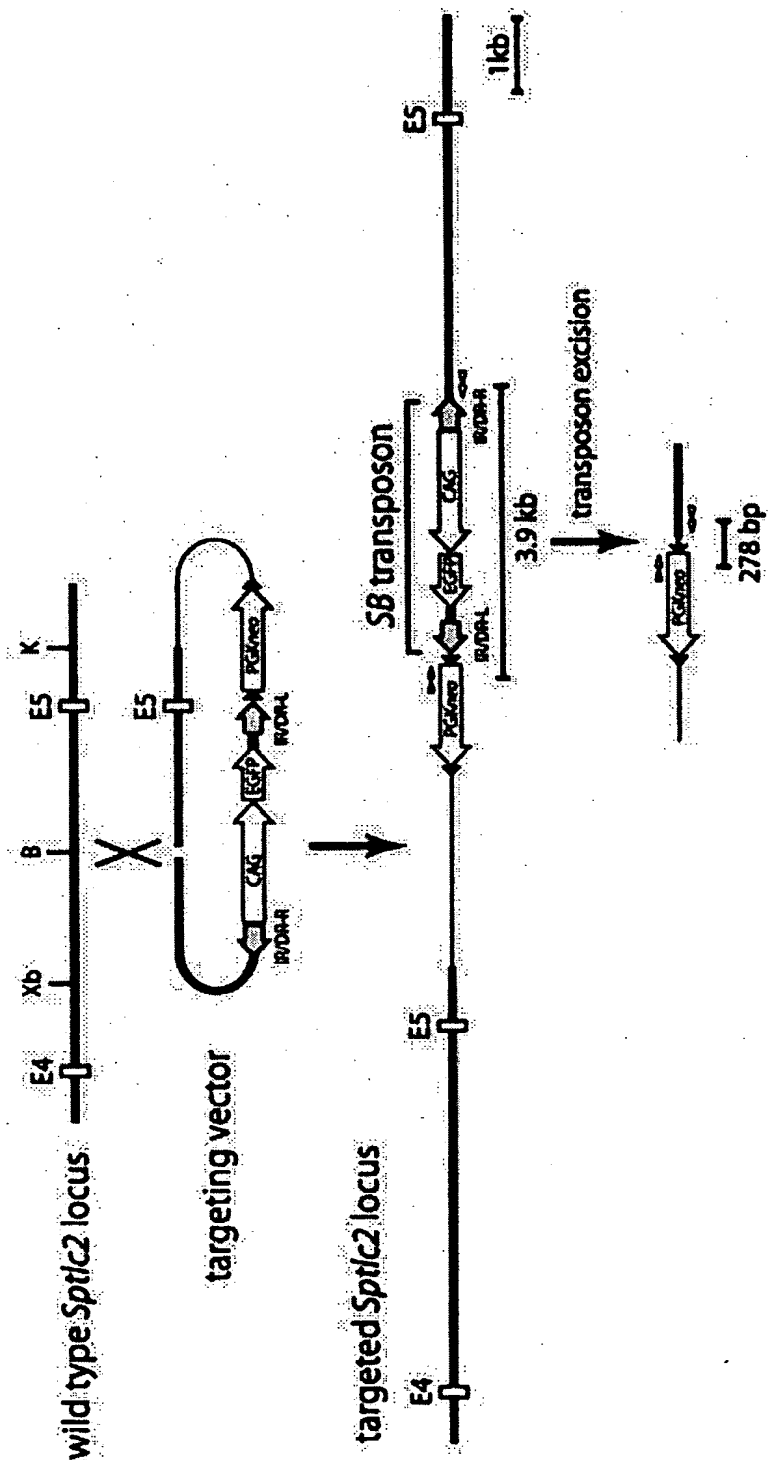


Fig. 1B

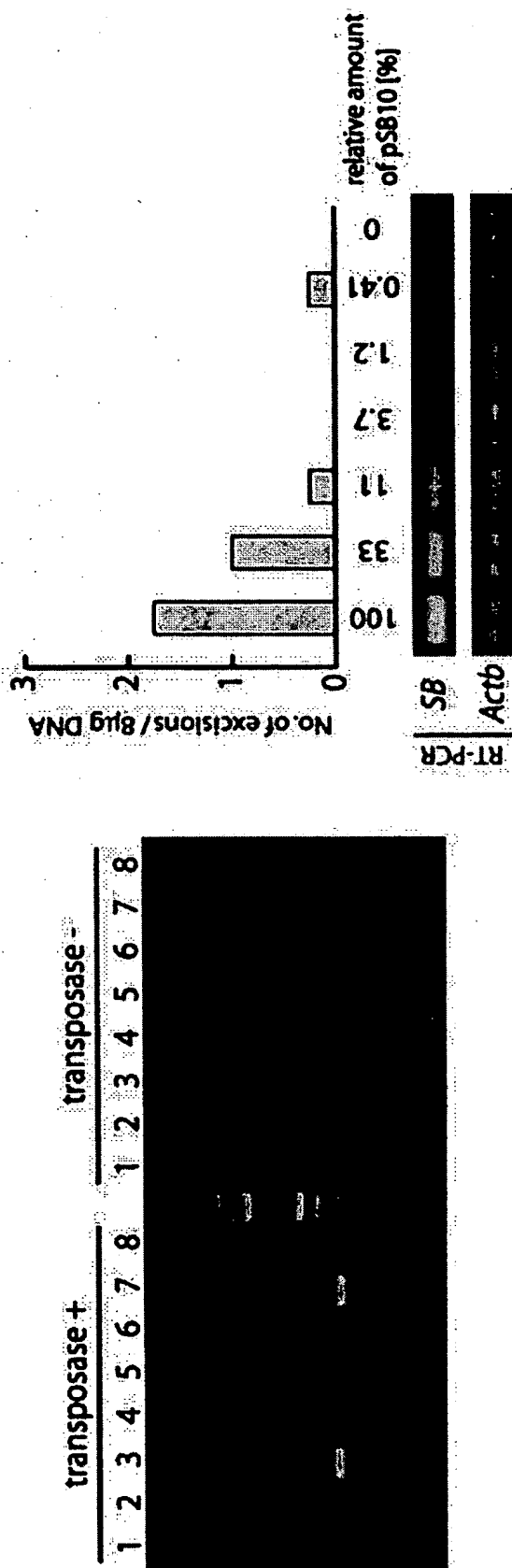


Fig. 1C

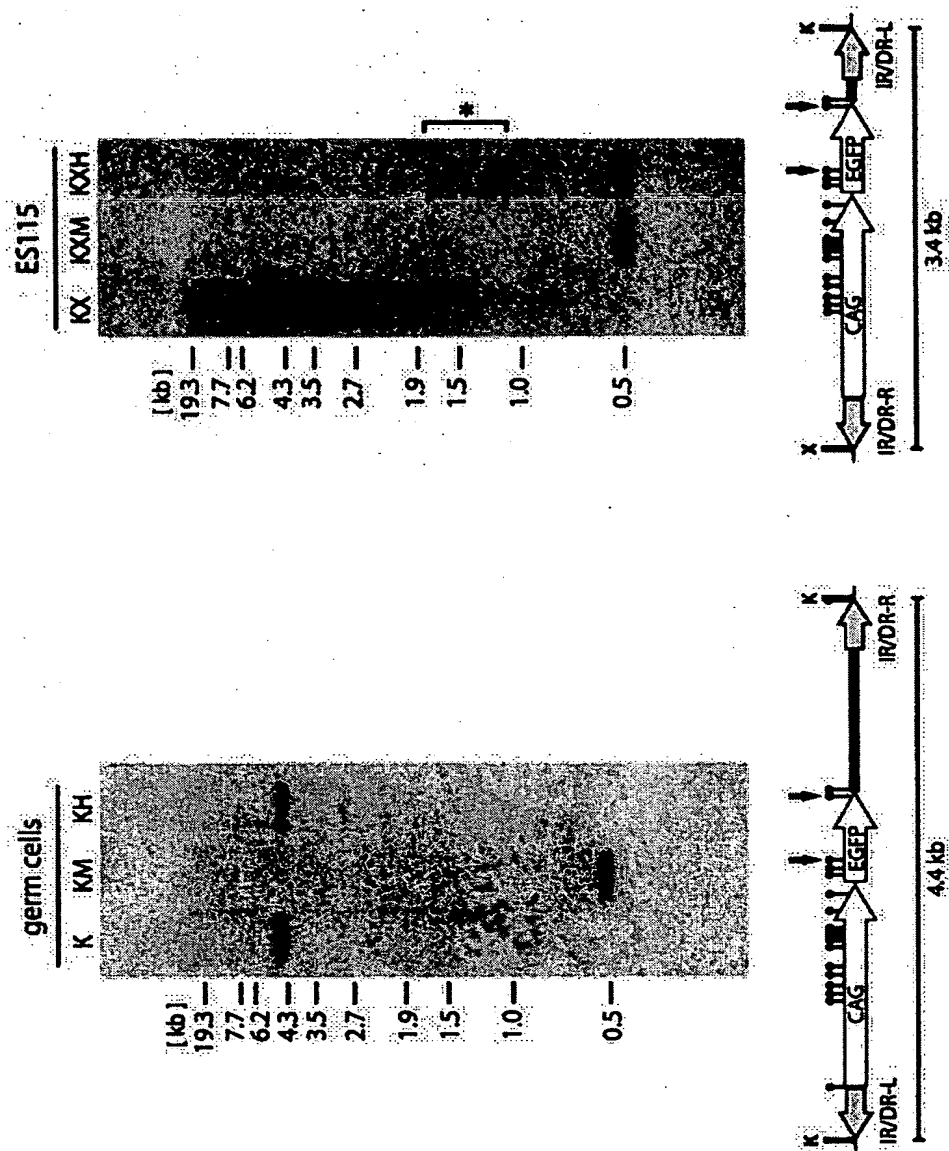


Fig. 1D

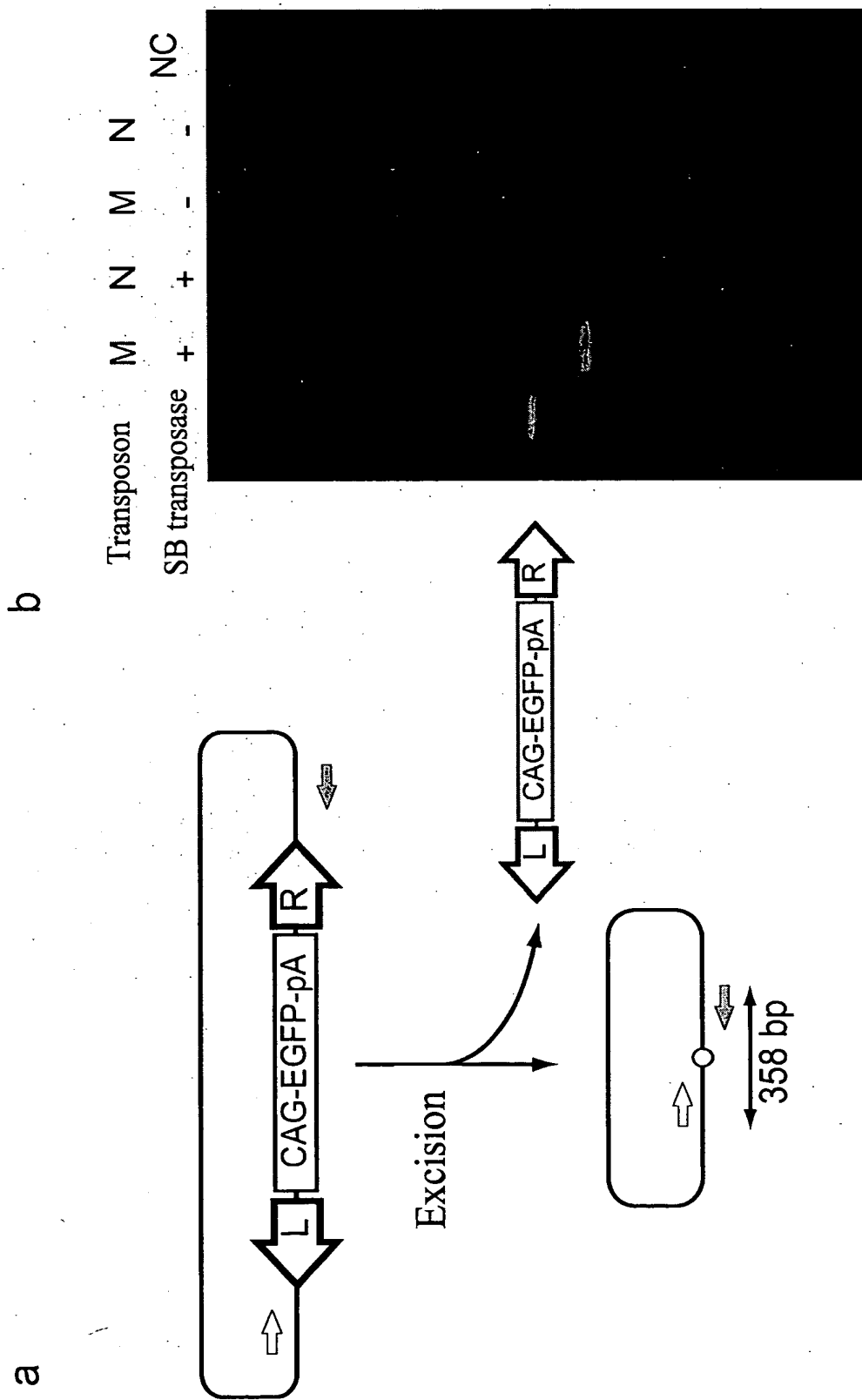


Fig. 2A

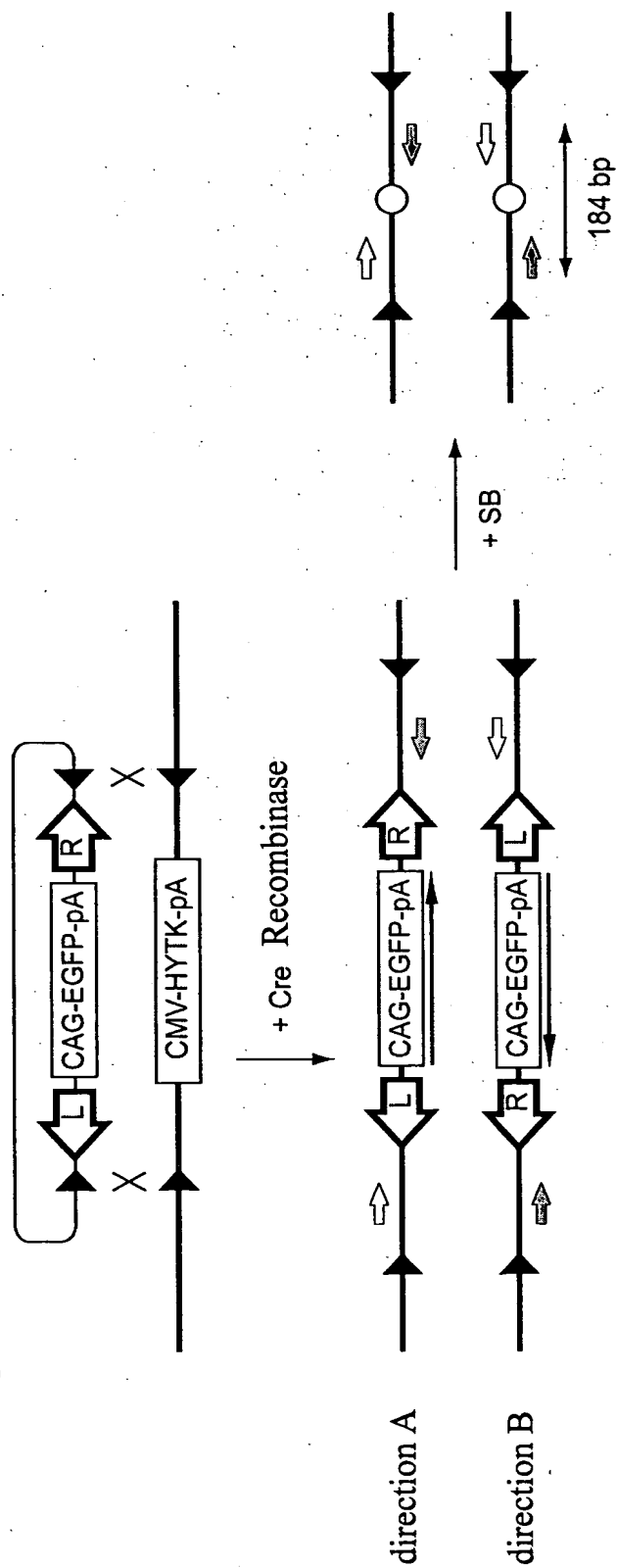
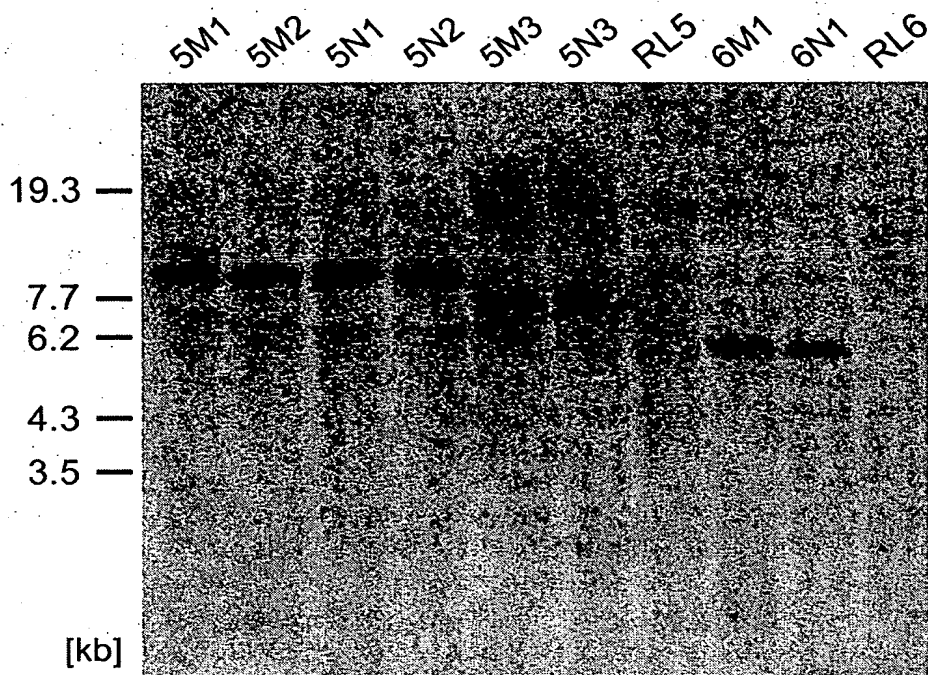


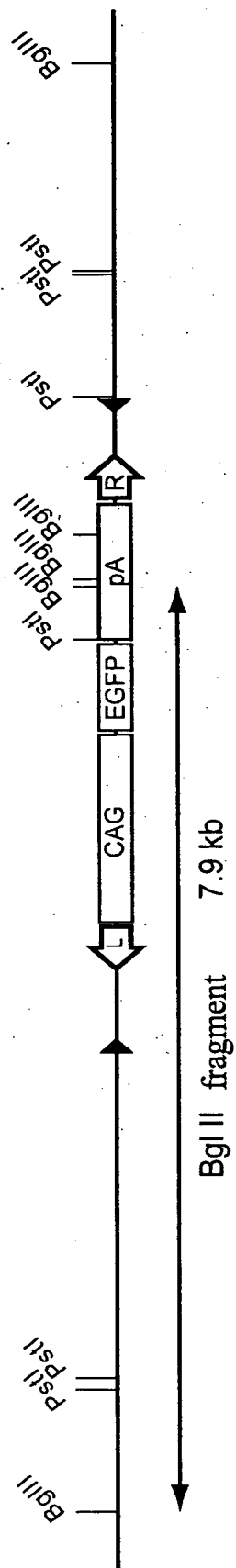
Fig. 2B



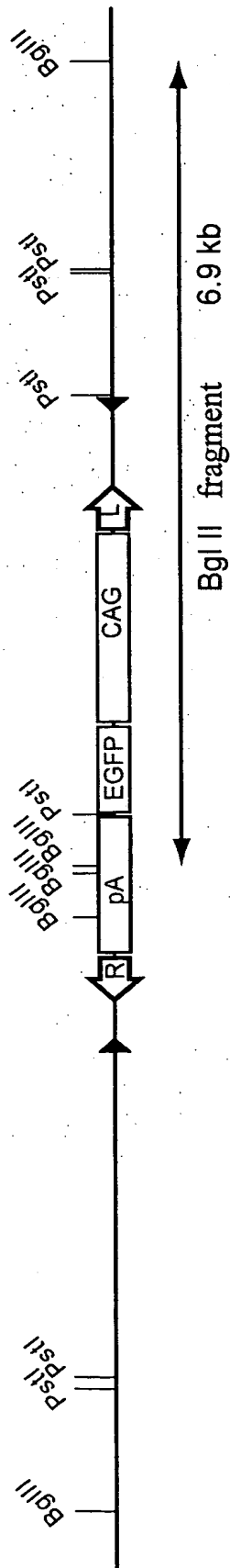
7/30

Fig. 2C

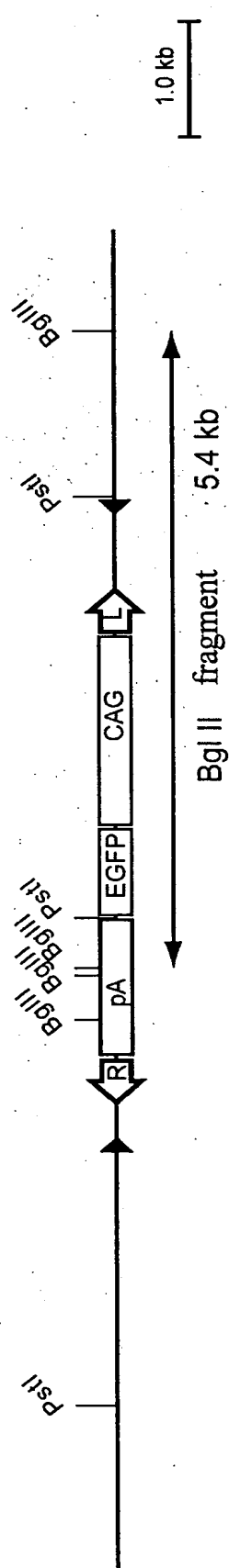
RL5- direction A

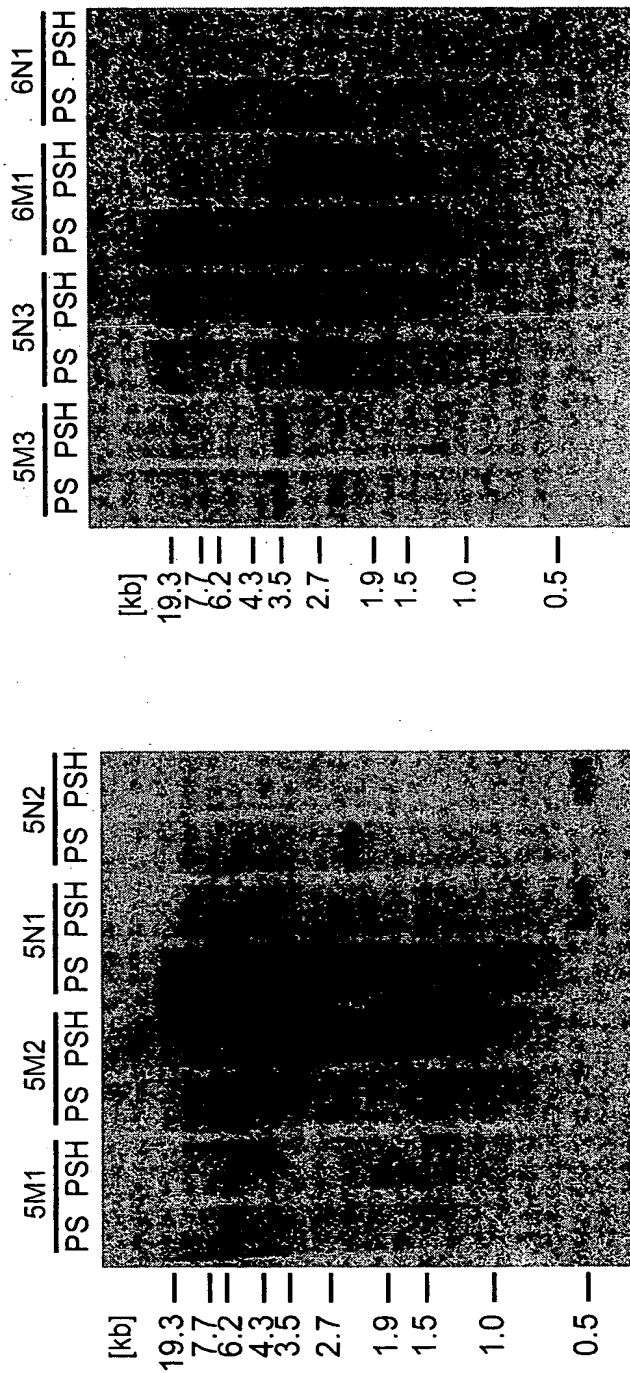


RL5- direction B



RL6- direction B







9/30

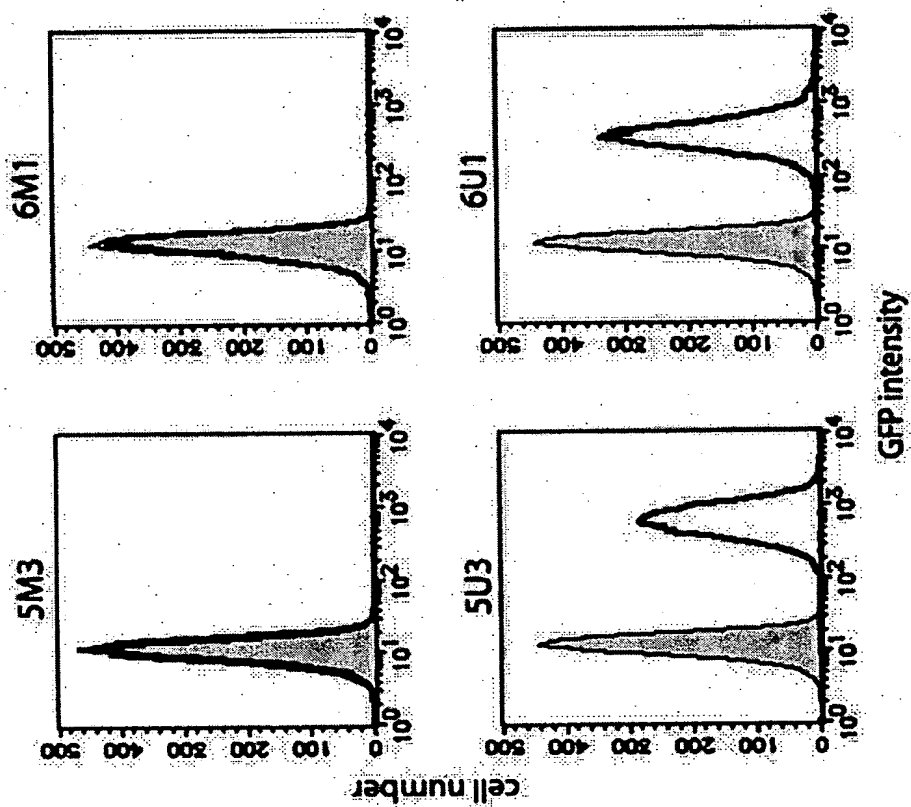
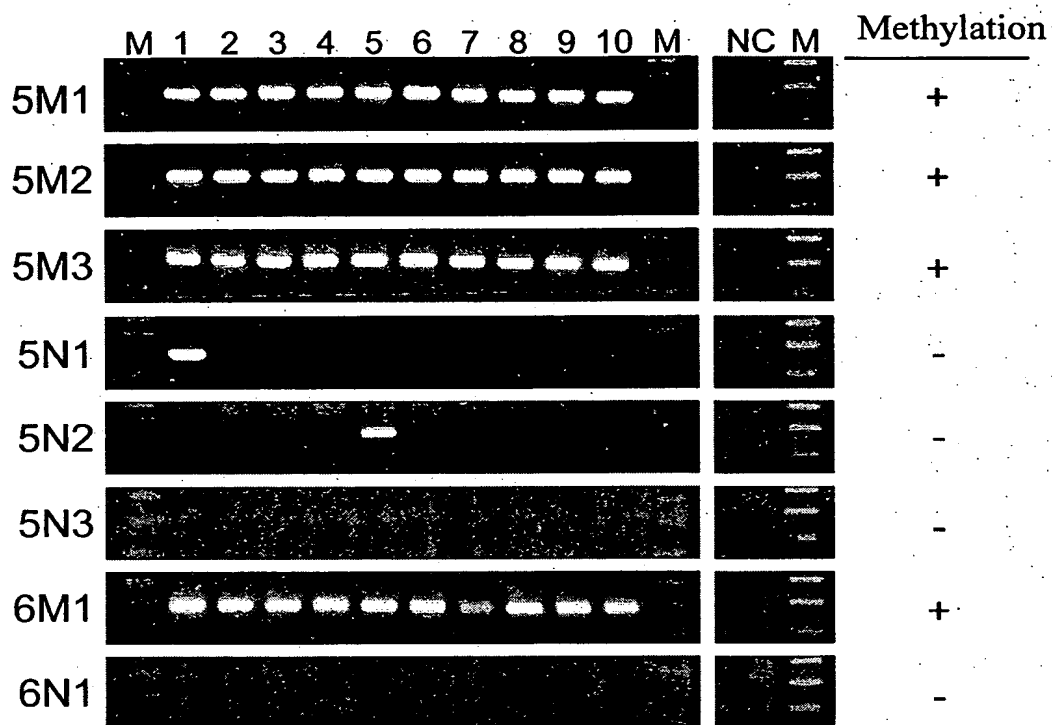


Fig. 2E

10/30

Fig. 3A



1 $\mu$ g template											parental done			
M	1	2	3	4	5	6	7	8	9	10		M		
5M1	[band]										NC	M	+	RLS
5M2	[band]										NC	M	+	RLS
5U1	[band]										NC	M	-	RLS
5U2	[band]										NC	M	-	RLS

1 $\mu$ g template											10 ng template											mCpG	parental clone
M	1	2	3	4	5	6	7	8	9	10	M	1	2	3	4	5	6	7	8	9	10		
5M3																						+	RL5
5U3																						-	RL5
6M1																						+	RL6
6U1																						-	RL6

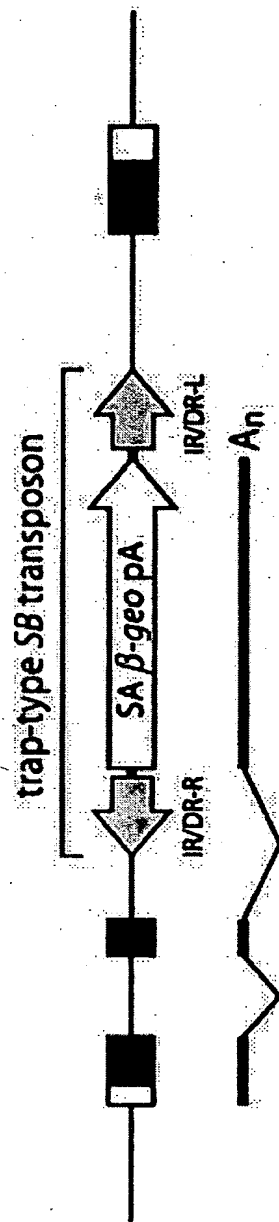


Fig. 4A

Fig. 4B

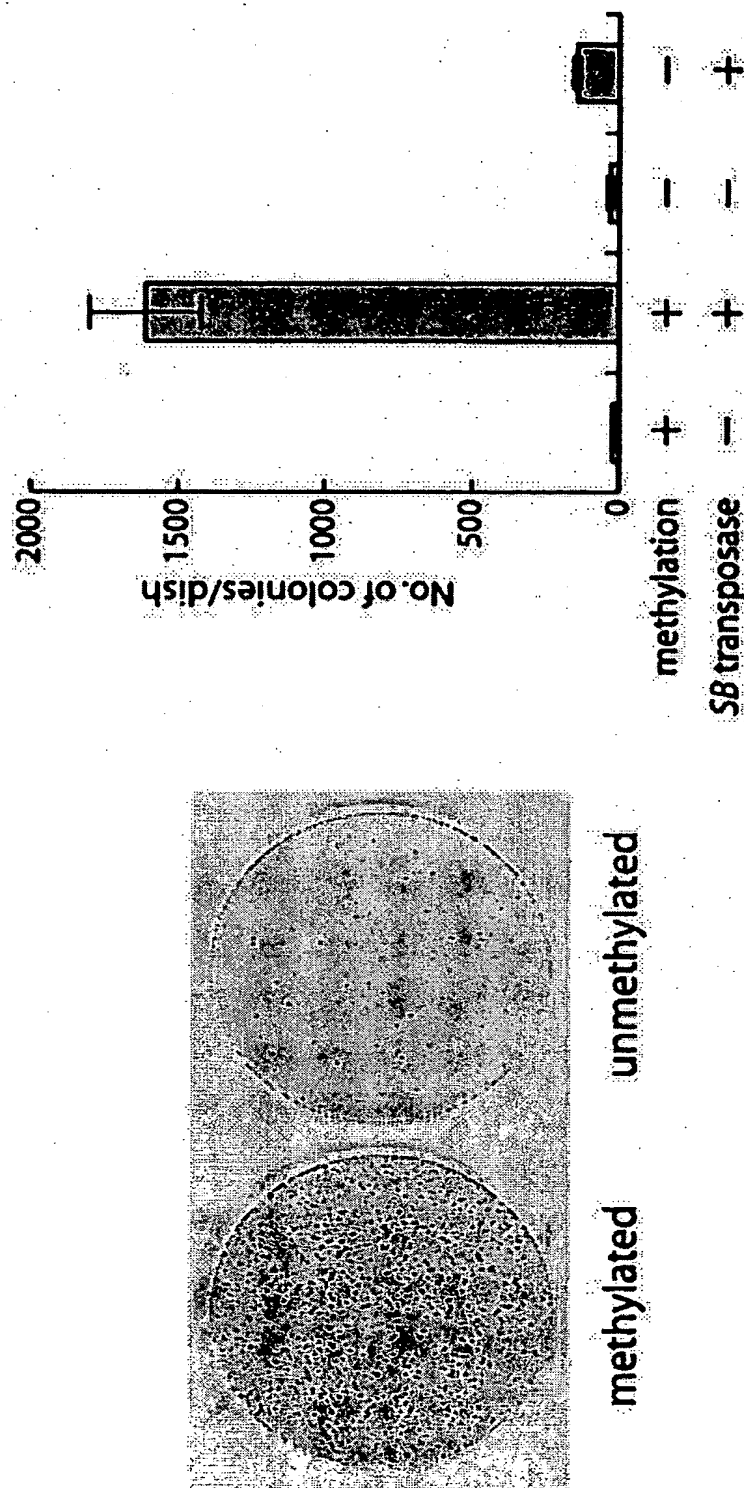
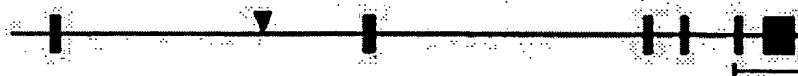
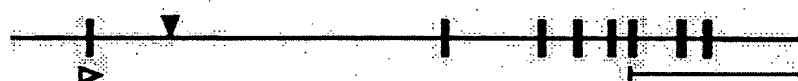


Fig. 4C

M1: Chr. 10, NM\_172508



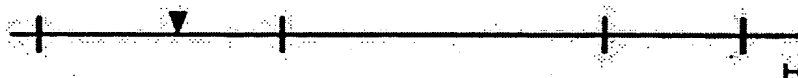
M2S: Chr. 7, ENSMUST49387



M2L: Chr. 8, ENSMUSESTT33450



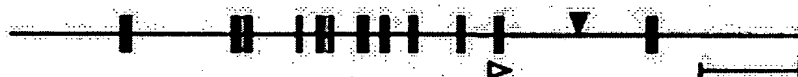
M3: Chr. 16, ENSMUSESTT27446



M4: Chr. 19, Pten



N1: Chr. 1, ENSMUST27914



N6: Chr. 16, ENSMUSESTT26711

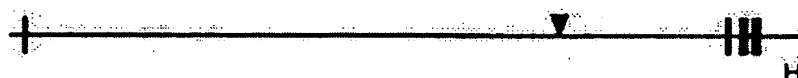


Fig. 4D

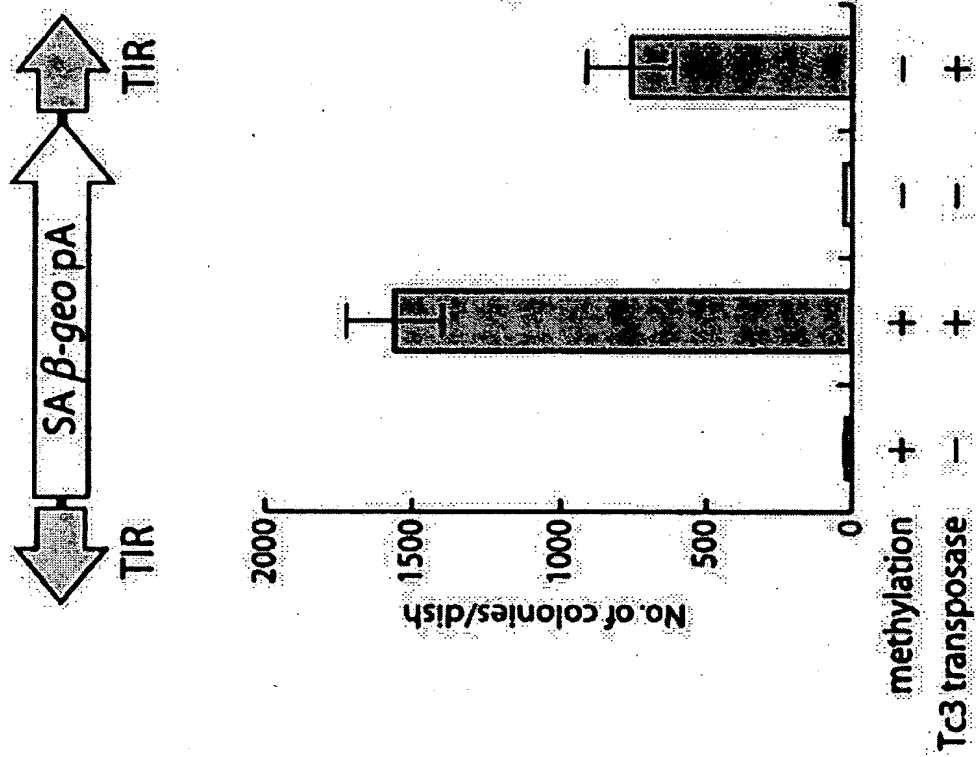




Fig. 5A

CLUSTAL W (1.81) Multiple Sequence Alignments

Sequence type explicitly set to DNA  
Sequence format is Pearson  
Sequence 1: X01005 1610 bp  
Sequence 2: Z29098 1773 bp  
Sequence 3: Z29102 1717 bp  
Sequence 4: U11641 1263 bp  
Sequence 5: U11652 1296 bp  
Sequence 6: L48685 1455 bp  
Start of Pairwise alignments  
Aligning...  
Sequences (5:6) Aligned. Score: 3  
Sequences (3:4) Aligned. Score: 3  
Sequences (1:2) Aligned. Score: 9  
Sequences (3:5) Aligned. Score: 3  
Sequences (4:5) Aligned. Score: 95  
Sequences (1:3) Aligned. Score: 9  
Sequences (3:6) Aligned. Score: 10  
Sequences (4:6) Aligned. Score: 3  
Sequences (1:4) Aligned. Score: 1  
Sequences (2:3) Aligned. Score: 99  
Sequences (1:5) Aligned. Score: 3  
Sequences (2:4) Aligned. Score: 3  
Sequences (1:6) Aligned. Score: 2  
Sequences (2:5) Aligned. Score: 3  
Sequences (2:6) Aligned. Score: 10  
Guide tree file created: [clustalw.dnd]  
Start of Multiple Alignment  
There are 5 groups  
Aligning...  
Group 1: Sequences: 2 Score:32613  
Group 2: Delayed  
Group 3: Delayed  
Group 4: Sequences: 2 Score:22721  
Group 5: Sequences: 4 Score:12095  
Sequence:6 Score:13071  
Sequence:1 Score:12960  
Alignment Score 47622  
CLUSTAL-Alignment file created [clustalw.aln]  
CLUSTAL W (1.81) multiple sequence alignment:

Z29098	CGAGCCCCAACCACCTATTAATTCGAACAGCATGTTTTTTTGCAGTGC6CAATGTTTAAC
Z29102	_____TAAC
U11641	_____
U11652	_____
L48685	_____
X01005	_____

Z29098	ACACTATATTATCAATACTACTAAAGATAACACATACCAATGCATTTCTCAAAAGAGA
Z29102	ACACTATATTATCAATACTACTAAAGATAACACATACCAATGCATTTCTCAAAAGAGA
U11641	_____
U11652	_____

Fig. 5B

L48685  
X01005  
CAGTTGAAGTC—GGAAG  
CAGTGCTGGCCAAAAAGA

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005  
ATTTTATTCTCTTCACGACGAAAAAAAAGTTTGTCTATTTCCAACAACAACAAAAAT  
ATTTTATTCTCTTCACGACGAAAAAAAAGTTTGTCTATTTCCAACAACAACAAAAAT

TTTACATACACTTAAGTTGAGTCATTAAA—ACTCGTTTTTCACTACACCACAAAT  
TATCCA—CTTTTGGTTTTTGTGTATA—CTTTTTCTCAAGCATCCATTGAC

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005  
ATGAGTAATTTATTCAAACGGTTTGTCTAAGAGATAAGAAAAAGTGACCACTATTAATT  
ATGAGTAATTTATTCAAACGGTTTGTCTAAGAGATAAGAAAAAGTGACCACTATTAATT  
AACATGT  
ATTAGGT  
TTC—TTGTTAA—CAAACAAT—AGTTTTGGCAAGTCAGTTAGGACATCTACTT  
TTG—AATTTTTCCGTGTGCATAAAGCGAAATGTTACGCAAAATTGCGGACCAA—ACAT  
\* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005  
CGAACGCGGCGTAAGCTTACCTTAATCTCAAGAAGAGCAAAACAAAAGCAACTAATGTAA  
CBAACGCGGCGTAAGCTTACCTTAATCTCAAGAAGAGCAAAACAAAAGCAACTAATGTAA  
TGGCTG—ATAAGTCC—CGGTTTGACAC—TAGTATTAATGCA—  
TGGCTG—ATAAGTCC—CGGTTTGACACATAGATGGCTGCTAGTATTAATGCA—  
TGTGATGACACAAGT—CATTTTTCCAACAATTGT—TTACAGACAGATTATTTCA  
TACATGATTATCGATTTTTCTGAATTTTATTTCAATTT—TTGATTTTTCTGTTTTTC  
\* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005  
CGGAATCATTATCTAGTTATGATCTGCAATAAT—GTCACAATACAGCATGCAAAAA  
CGGAATCATTATCTAGTTATGATCTGCAATAAT—GTCACAATACAGCATGCAAAAA  
TATTATTTTATATAGGACCAACCTTCAAATGATTCGTGTGCAAAATTTGACGTC  
TATTATTTTATATAGTACCAACCTTCAAATGATTCGTGTGCAAAATTTGACGTCGTAAAG  
CTTATAATTCAGTGTATCACAAT—CCAGTGG—GTCAGAAATTTACATACA—  
AATTTTCATTATTTTTTTGAATTTATCAATAAACGCACTCTGTTGTTGCACTGG—A  
\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005  
AATTTTAGATTGCTGCA—GATCAGTAGAAGTTTAGCAACGATGGTTCGTGGTAAACCTA  
AATTTTAGATTGCTGCA—GATCAGTAGAAGTTTAGCAACGATGGTTCGTGGTAAACCTA  
—AATTAGTTTGTGAGA—GCAACTTTTGTATTGTGAAGAAAA  
TCAATTAGTTTGTGABATAGAGCGTCTTTTGTGAAGCAACTTTTGTATTGTGAAGAAAA  
—CTAAGTTGACTGTG—CCTTAAA—CAGCTTGGAAAAATCCAG—AAATGA  
TTTGTGTTGGTGAATAAT—TATTTTAAAGGTATGGTAAATCTGTTGGGTGTAAAAATC  
\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005  
TTTCTAAAG—AAATCAGAGTATTGATTAGGGATTATTTTAAATCTGGAAG  
TTTCTAAAG—AAATCAGAGTATTGATTAGGGATTATTTTAAATCTGGAAG  
TGGAAAAAATTTCAATTCGAATTCGTGTTTTGATAAAATACTGTTTTCTGAAGGGAAAA  
TGGAAAAA—AGGAATTTCTGTTTTGATAAAATACTGTTTTCTGAAGGGAAAA  
TGTGATGGC—TTTAAAGCTTC—TGATAGACTAATGACATCATTGAG  
TTTCTTGG—ACGTCAAGAAAGCCATTGTAG—CTGGCTTCGAACAAGGAAT  
\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005  
ACACTTACGGAGATAAGCAAGCAATTAATTTGCCAAGTCGTCTGTGCATGGGGTGAAT  
ACACTTACGGAGATAAGCAAGCAATTAATTTGCCAAGTCGTCTGTGCATGGGGTGAAT  
AA—TGGGGTGG—AAGCAAAAAGTTGGCTTGATAATGATTTCCGGAAGCTGCCCCAA—  
AA—TACAGTGG—AAGCAAAAAGTTGGCTTGATAATGATTTCCGGAAGCTGCCCCAG—  
TCAATT—GGAGGTGTACCTGTGGATGATTT—CAAGGCTACCTTCA—AACGCAAT—  
ACCCAGCAAAAGCTCGCGCTGCAAAATCAACGTTCTCCGTGCACTATTTGGAAAGTAATC

Fig. 5C

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005

ACAAATTTTCAAAAAA-AATG66AATATTGAAAAATAA-CA-TT6CGAATAGAGGCCGAA  
ACAAATTTTCAAAAAA-AATG66AATATTGAAAAATAA-CA-TT6CGAATAGAGGCCGAA  
GGAAATCAATAATAATTGATTG6TATGCAAAATTCAAGCG-AGGTGAAATGAGCACGGA  
GGAAATCAACAATAATTGATTG6TATGCAAAATTCAAGCG-TG6TGAAATGAGCACGGA  
GCCTCTTTGCTTGACATAATG6GAAAAATCAAAAGAAATCAGCCAAACCATGGGACCAG  
AAGAAGTACCAAACTGAGGTGABTTGAAAAATATTATTTTTAATAATAATGTTTGA

\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005

CATCAGCAA-TAACACCCCGCAGCAAAAGACAA-CTGGCCAAAATTGTTAAGGCTGAT  
CATCAGCAA-TAACACCCCGCAGCAAAAGACAA-CTGGCCAAAATTGTTAAGGCTGAT  
GGACGGTGA-ACGCAAGTGGACGCCGAAAG-AG-6TGGTTACCGACGAAAA-  
GGACGGTGA-ACGCAAGTGGACGCCGAAAG-AG-6TGGTTACCGACGAAAA-  
CAGCCGTCA-TACGCTCAGGAATGAGACGCATTCTGTCTCTAGAGATAAA-  
AATCCGTGCTTTGAGAATCTGCGCCGCGACGGCT-CGAGTACAACCATAGGATGGAT

\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005

CGTCGCCAATCTTTGAGAAATTTGGCTTCTAAGTGGTCGCA-GCAATTGGCAAACT  
CGTCGCCAATCTTTGAGAAATTTGGCTTCTAAGTGGTCGCA-GCAATTGGCAAACT  
CATCAAAAAATCCACAAAAT-GATTTTGAATGACCGTAAAAATGAAGTTGATCSAGAT  
CATCAAAAAATCCACAAAAT-GATTTTGAATGACCGTAAAAATGAAGTTGATCSAGAT  
CAT-ACTGTGGTGGCAAAAGT-GCAATCAATCCAGAACGACAGCAAAAGGACCT  
CGC-AACATCCTCCGATCAGCA-AGAGAAGATCCGCATAG-GACCGCCACGGATAT

\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005

GTCAAGCBAGAGTGGACGCGACAAATTAAGATAT-TGGATATGTTTTATAAAGT  
GTCAAGCBAGAGTGGACGCGACAAATTAAGATAT-TGGATATGTTTTATAAAGT  
AACAAA-GGCTTTAAACATATCAAA-GGAACGTGT-TGGTCATATCATTATCAAA-  
AGCAGA-GGCTTTAAAGATATCAAA-GGAACGTGT-TGGTCATATCATTATCAAA-  
TGTGAA-GATGCTGGAGAAAACAGGTATGAATGTTTCTATATCCACAGTAAAAACGAGTC  
-TCAATGATTATAAGTTCTCCAAATGAACCTGTAC-CAAGTAAACGAACTGTTCTGTC

\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005

ATGTTTTGTTATTACCTGTGCATCGTACCCAATAACTTACTCGTAATCTTACTCGTAGGC  
ATGTTTTGTTATTACCTGTGCATCGTACCCAATAACTTACTCGTAATCTTACTCGTAGGC  
-TATTTGGATAT-GCGGAAGCTCTGTGCAAAATG66TGCCGCGCBAAGCTCAGAT-TTGAC  
-TATTTGGATAT-GCGGAAGCTCTGTGCAAAATG66TGCCGCGCBAAGCTCAGAT-TTGAC  
CTATATCAGATAACCTGAAAGGC-CGCTCAGCAAGGAAGAGCCA-CTGCTCCAAAAC  
GACGTTTACAGCAAGCAGGACTACACGGACGA-AAGCCAGTCAAGAAACGTTTATCAGT

\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005

CAAGG-AAAAACCTTGCTTACGCTTCGTCAAAAAAAGAGC6TTTGCAATGGG-CTCG  
CAAGG-AAAAACCTTGCTTACGCTTCGTCAAAAAAAGAGC6TTTGCAATGGG-CTCG  
CAAAA-ACAACAACGTGTTGATGATTCT-GAGCGGTGTTTGAGGCTGT-TAAC  
CAAAA-ACAACAACGTGTTGATGATTCT-GAGCGGTGTTTGAGGCTGT-TAAC  
CGCCATAAAAAAGCCAGACTACGTTTGCAACTGCACATGGGAGCAATATGTTACTTTT  
AAGAA-AAATCGCATG6CTCGA6TTGCGTGGGCAAAAGC-GCATCTTCGTTGGGACGTC

\* \* \* \* \*

Z29098  
Z29102  
U11641  
U11652  
L48685  
X01005

GGAAAGGATGCTTGGACTCAAAGGCAATGGGATACCATCATATTGAGGATGAAGCTAA  
GGAAAGGATGCTTGGACTCAAAGGCAATGGGATACCATCATATTGAGGATGAAGCTAA  
TCGTAATACACCCAGTTTTCGCTCGATATG-TAAGATGGATGAAACATGGCTCCATC  
TCGTAATACACCCAGTTTTCGCTCGATATG-TGACAATGATGAAACATGGCTCCATC  
TGGAGAAATGCTCTCTCTGCTGCTGATGAA-AAAAAATGAACTATTTGGCCAT  
AGGAATGGGCTAAACACATCTGCTGACGAA-AGCAAGTTCAATTTGTTGGGAGT

\* \* \* \* \*

Fig. 5D

Z29098 ATTTGATGTTAGTGTGCGCGATACGAGAAAACGCGTCATCCGTAAAGAGGTCAGAAACATA  
Z29102 ATTTGATGTTAGTGTGCGCGATACGAGAAAACGCGTCATCCGTAAAGAGGTCAGAAACATA  
U11641 ACTACACTCCTGAGTTCBATCAACAGTCGCGTGAATGGACAGCGACCGGT—GAACCGTC  
U11652 ACTACACTCCTGAGTTCBAACAGACAGTCGCGTGAATGGACAGCGACCGGT—GAACCGTC  
L48685 AATGACCATCCTTAT—GTTTGGAGGAAAAAGGGGAGCTTSCAAGCCG—AAGATCA  
X01005 GATGGAATTCCTG—GGTACGTCCTCTGTTGGCTCTAGGTAAGTCTCCAAAGTA  
\* \* \*

Z29098 CCATAAAGACTGCCTTAAAAGAACAAAGTTTCTGCGAGCACTATGATGAGGATG  
Z29102 CCATAAAGACTGCCTTAAAAGAACAAAGTTTCTGCGAGCACTATGATGAGGATG  
U11641 TCCGAAG—CGTGGAAAGACTCAAAAGTCCGCTGGCAAAGTAATGGCTCTGTTTT  
U11652 TCCGAAG—CGTGGAAAGACTCAAAAGTCCGCTGGCAAAGTAATGGCTCTGTTTT  
L48685 CCATC—CCAAGCGTGAAGCAGCGGG—TGGCAGCATCATGTTGTGGGGTG  
X01005 TCAATGC—CCAACCGTTAAGCATGGAGG—TGGGAGCGTCATGGTGTGGGGTG  
\* \* \* \* \*

Z29098 TATGCTGCGAAAGGATTAGGAAAACCTTCATTTCATTGAAGGACAGTTAATGCTGAAAA  
Z29102 TATGCTGCGAAAGGATTAGGAAAACCTTCATTTCATTGAAGGACAGTTAATGCTGAAAA  
U11641 TTGGAAATGCGCATGGAATAATTTTATCGATTATCTTGAGAAAGGAAAAACCATCAACAG  
U11652 TTTCGATGCGCATGGAATAATTTTATCGATTATCTTGAGAAAGGAAAAACCATCAACAG  
L48685 CTTTGCTGCAAGGAGGACTGGTGCACCTCACAAAATAGATGGCATCATGACAAAAGAAAA  
X01005 CTTCAACGACACTTCATGGGCCCACTAAGGAGAAATCCAAAGCATTATGGATCGTTTTCA  
\* \* \*

Z29098 ATATATTAATATTTTACAAGATAGTTTGTGCCATCAATACCAAACTATTAGATTGCGG  
Z29102 ATATATTAATATTTTACAAGATAGTTTGTGCCATCAATACCAAACTATTAGATTGCGG  
U11641 —TGACTATTATATGGCGTTATTGTAGCGTTTGAAGGTCGAAATCGCGGCAAAATGG  
U11652 —TGACTATTATATGGCGTTATTGTAGCGTTTGAAGGTCGAAATCGCGGCAAAACGG  
L48685 TTATGTGGCTATATTGAAGCAACATCTCAAGACATCAGTCAGGAAAGTTCAAGCTTGGTCA  
X01005 ATACGAAAACATCTTTGAACTACAATGCGACCGTGGGCACCTCAAAATGTGGGCCGTGG  
\* \* \*

Z29098 TGAATTCAGTTTTAGCAGGACGAGCATCATCGCAC—ACAGCCAAGCGAACCAAAA  
Z29102 TGAATTCAGTTTTAGCAGGACGAGCATCATCGCAC—ACAGCCAAGCGAACCAAAA  
U11641 —CCCCATATGAGAAAGAAAAAGTGTGTTCCAGCAAGCAATGACCGTGGCCAAA  
U11652 —CCCCATATGAGAAAGAAAAAGTGTGTTCCAGCAAGCAATGACCGTGGCCAAA  
L48685 CAAATGGGTCTTCCAAATGGACAATGACCTCAAGCAT—ACTTCCAAAGTTGTGGCAA  
X01005 C—TTCGTGTTTACGAGGATTAACGATCCTAAGCAT—ACTTCTCTTCATGTGCGTT  
\* \* \* \* \*

Z29098 ATTGGCTGCAATATAATCAAATGGAAGTTTTAGATTGGCCATCAAATAGTCCAGATCTAA  
Z29102 ATTGGCTGCAATATAATCAAATGGAAGTTTTAGATTGGCCATCAAATAGTCCAGATCTAA  
U11641 GTCAGTAAGAACGATGGCAAA—AATTCATGAATTGGGCTTCGAAATGCTTCCCCACCC  
U11652 GTCATTGAGAACGATGGCAAA—AATTCATGAATTGGGCTTCGAAATGCTTCCCCACCC  
L48685 AATGGCTTAAGGTCAACAAAGTCAAGGTATTGGAGTGGCCATCACAAAGCTGTGACCTCA  
X01005 CATGGTTTCAACGTCGTATGTGCAATTTGCTGATTTGGCCAAAGTCAGTCTCCGAGTTGA  
\* \* \* \* \*

Z29098 GCCCAATTGAAAAATATTTGGTGGCTAATGAAAAACAGCTT—CGAAAT—GAGCC—ACA  
Z29102 GCCCAATTGAAAAATATTTGGTGGCTAATGAAAAACAGCTT—CGAAAT—GAGCC—ACA  
U11641 ACTATATTCTCAGATCTGGCCCGCAGCGAATTTTCTTGT—TCTCA—GACCT—CAA  
U11652 ACCGTATTCTCAGATCTGGCCCGCAGCGAATTTTCTTGT—TCTCA—GACCT—CAA  
L48685 ATCCTATAGAAAAGGAGGAATGAGCCAAATTCACCAACTTATTGTGG—AAGCTTGTG  
X01005 ATCCAATAGAGCATTTGTGGGAAGAGTTGGAAGAGCTCTTGGAGGTATTGCGGCT—TCA  
\* \* \*

Z29098 AAGGAATATTTCTGACTTGAAAAATCAAGTTGCAAGAGATGTGGGACTCAATTTCTCAAGA  
Z29102 AAGGAATATTTCTGACTTGAAAAATCAAGTTGCAAGAGATGTGGGACTCAATTTCTCAAGA

Fig. 5E

U11641 AAGGGATGCTCGCAGGGAAAAAATTGGCTGCAATGAA-----GAGG  
U11652 AAGG-ATGCTCGCAGGGAAAAAATTGGCTGCAATGAA-----GAGG  
L48685 GAAGGCTACTCGAAATGTTTGACCCAAGTTAAACAATTT-----AAAG  
X01005 AATGCAGATGCCAAATTC--AACCAGTTGAAAAACGCTTGGAAAGCTATCCCATGTCA  
\* \* \* \* \*

Z29098 GCATTGCAAAAAATTTGTTAAGCTCAATGCCAAAAACGAGTTAAATGCGTAATGCAGGCCAA  
Z29102 GCATTGCAAAAAATTTGTTAAGCTCAATGCCAAAAACGAGTTAAATGCGTAATGCAGGCCAA  
U11641 TAATCGCCBAAAC--TAAGGCGTATTTTGAGGCAAAACCGTAAGAGTACTA-----CCA  
U11652 TGATCGCCBAAAC--TGAGGCGTATTTTGAGGCAAAACCGAAGGAGTACTA-----CCA  
L48685 GCAATGCTA-----CCAAATACTAATTTGAGTGTATGTTAACTTC--TGACCCA--CTGG  
X01005 GTTATTACAAAGCTGATCGA-CTCGATGCCACGTCGTTGTCAAGCTGTTATTGATGCAAA  
\* \* \* \* \*

Z29098 GGGCGACGTTACACAATTCTAATATTAATTAAATTATTGTTTTAAGTATGATAGTAAATC  
Z29102 GGGCGACGTTACACAATTCTAATATTAATTAAATTATTGTTTTAAGTATGATAGTAAATC  
U11641 AAATGGTATCAAAAAATTGGAAGGTCGTTATAATCGTGGTATCGCTCTTGA-AGGGGACT  
U11652 AAATGGTATCAAAAAATTGGAAGGTCGTTATAATCGTGGTATCGCTCTTGA-AGGGGACT  
L48685 GAATGTGATGAAGAAATAAAAGCTGAAATGAATCATTCTCTGACTATTATTCTG-----  
X01005 CGGATACGCGACAAAGTATTAAGCATAATTATGTTGT--TTTTAAATCCAATTGC--TC  
\* \* \* \* \*

Z29098 ACATTACGCCCGCTTCGAATTAATAGTGGTCACCTTTTTCTTATCTCTTAAGCAAACCGT  
Z29102 ACATTACGCCCGCTTCGAATTAATAGTGGTCACCTTTTTCTTATCTCTTAAGCAAACCGT  
U11641 ATGTTGAATAATAA--AAACGAATTTTGACAAAAAA--TGTTGTTTTCTTTGTAGACCGG  
U11652 ATGTTGAATAATAA--AAACGAATTTTGACAAAAAAATGTGTTTTCTTTGTAGACCGG  
L48685 ATATTTACATTTCTTAAATAAA--GTGGTGA--TCCTAACTGACCTTAAGACAGGGAAT  
X01005 ATATTCGGTACTT-----TAATTGTCATTTCTTGCAACCTCGGTTTTTCAATATTT  
\* \* \* \* \*

Z29098 TTGAATAAATTACTCATATTTTTGTTGTTGTTGGAAATAGAGCAAAACTTTTTTTTCGT  
Z29102 TTGAATAAATTACTCATATTTTTGTTGTTGTTGGAAATAGAGCAAAACTTTTTTTTCGT  
U11641 --GGACTTATCACCACCTGTTA-----  
U11652 --GGACTTATCAGCCAACCTGTTA-----  
L48685 C--TTTACTCGGATTAATGTCAGGAATGTGAAAAAGTGAAGTTAAATGTATTTG--GC  
X01005 C--TAGTTTTTCGATTTTTTTGAATTTTCTGAAAGTTTTTCAAATCTGTTGAACAT  
\* \* \* \* \*

Z29098 CGTGAAGAGAATAAAATTCTCTTTGAGACGAAATGCATTGGTATGTGTTATCTTTAGTAG  
Z29102 CGTGAAGAGAATAAAATTCTCTTTGAGACGAAATGCATTGGTATGTGTTATCTTTAGTAG  
U11641 -----  
U11652 -----  
L48685 -----  
X01005 TAAGGTGTATGTAACCTTCGACTTCAACTG-----  
TTTTG--ATGAATATTGTGTTTTAGATTTTGTGAACACTGTGTTGAAGTTTCAAAACA

Z29098 TATTGATAATATAGTGTGTTAAACATTGCGCACTGCAAAAAAACATGCTGTTCSAATTA  
Z29102 TATTGATAATATAGTGTGTTAAACATTGCGCACTGCAAAAAAACATGCTGTTCSAATTA  
U11641 -----  
U11652 -----  
L48685 -----  
X01005 AAATAACCACCTTAGAAAAAAGTTACACACAAAAAACCAAAAGTGGATATCTTTTGGCCA

Z29098 ATAGTGGTTGGGGCTCG  
Z29102 ATAGTGGTTGGGGCTCG  
U11641 -----  
U11652 -----

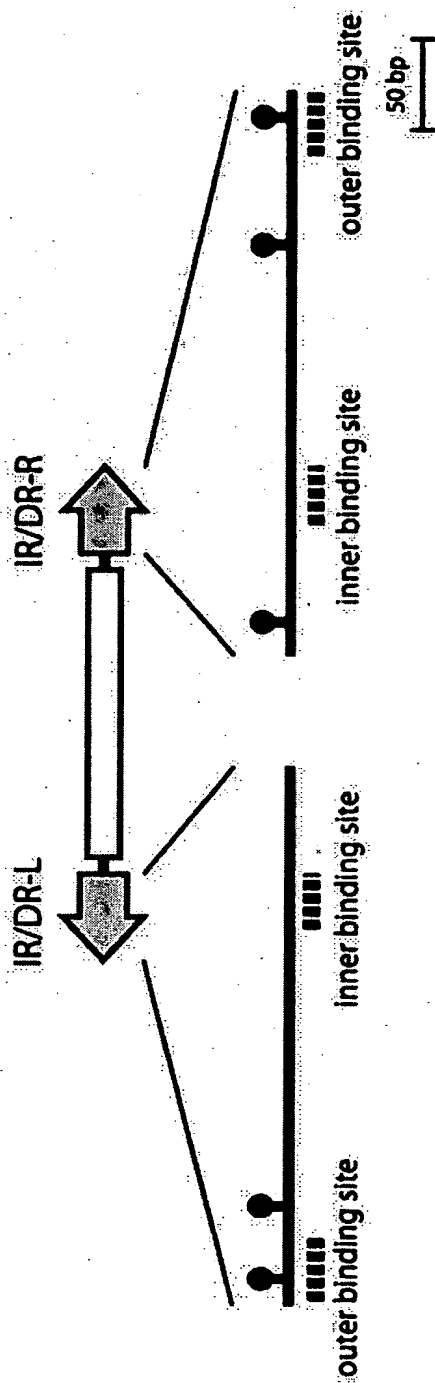
Fig. 5F

L48685  
X01005

GCAC78

(  
(  
X01005:0.47463,  
(  
U11641:0.02397,  
U11652:0.01879)  
:0.47911)  
:0.01531,  
(  
Z29098:0.00029,  
Z29102:0.00029)  
:0.42978,  
L48685:0.46683):

Fig. 6A



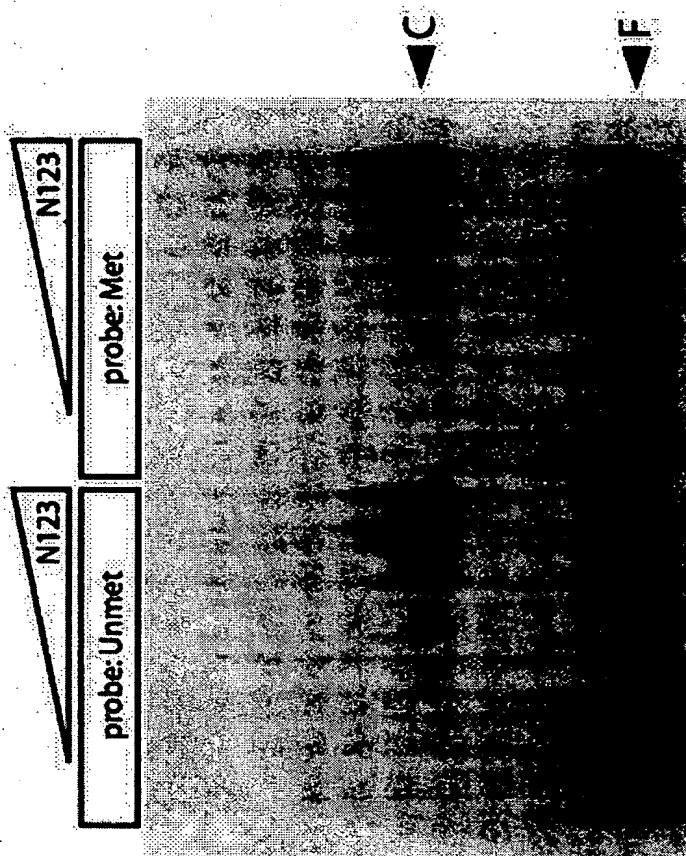


Fig. 6B



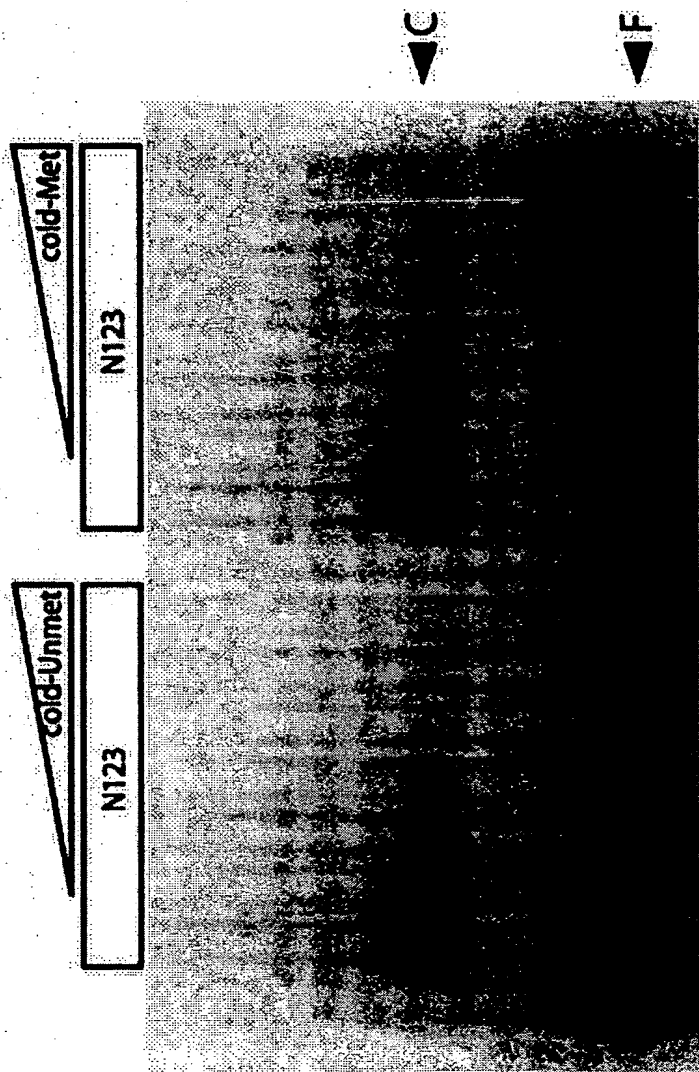


Fig. 6C

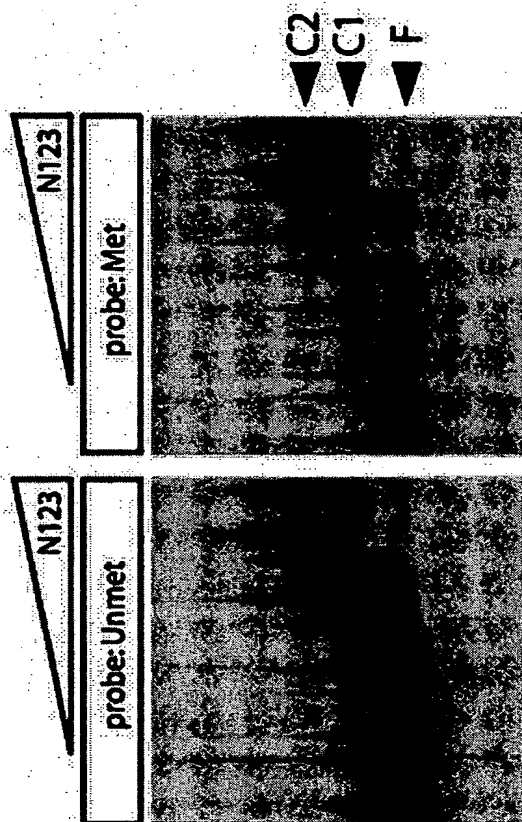


Fig. 6D

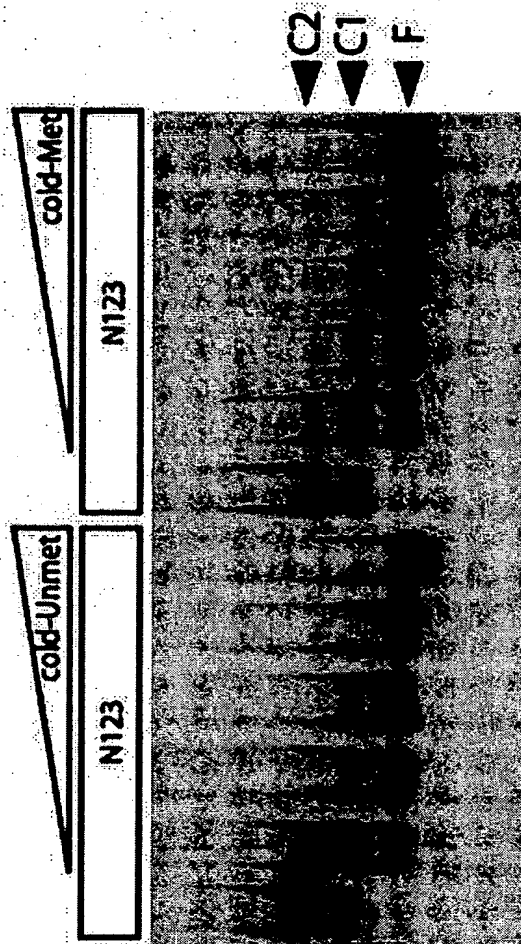


Fig. 6E

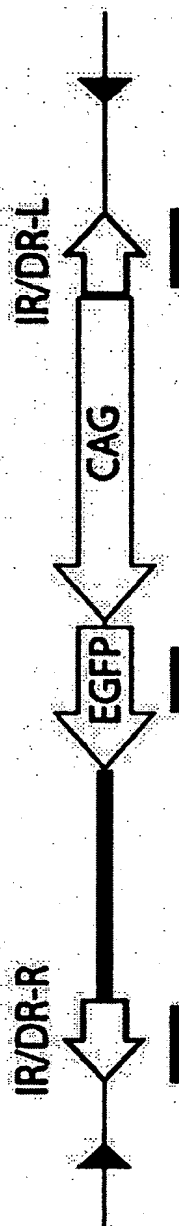


Fig. 7A

Fig. 7B

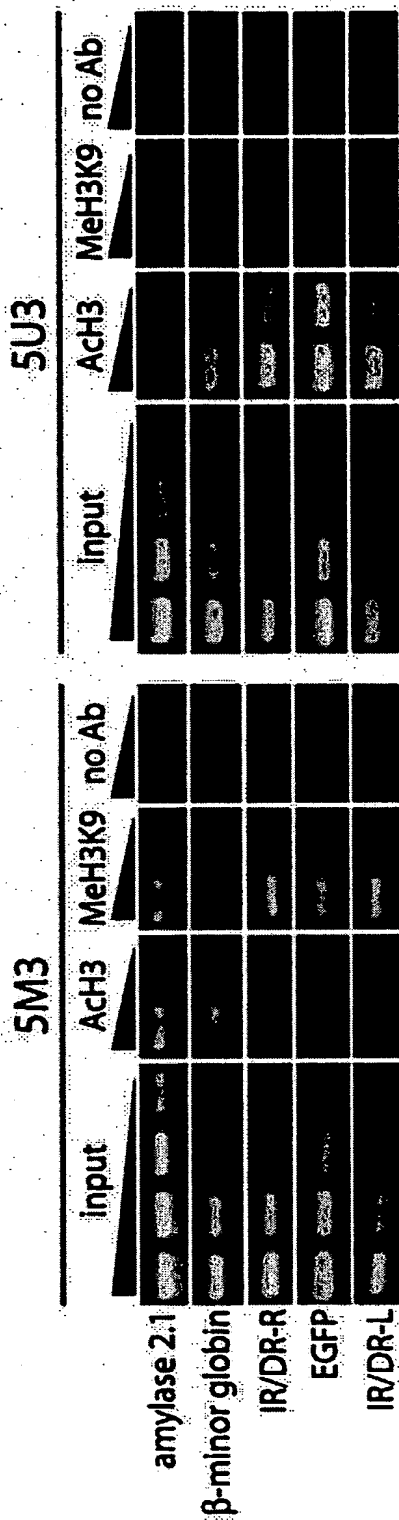
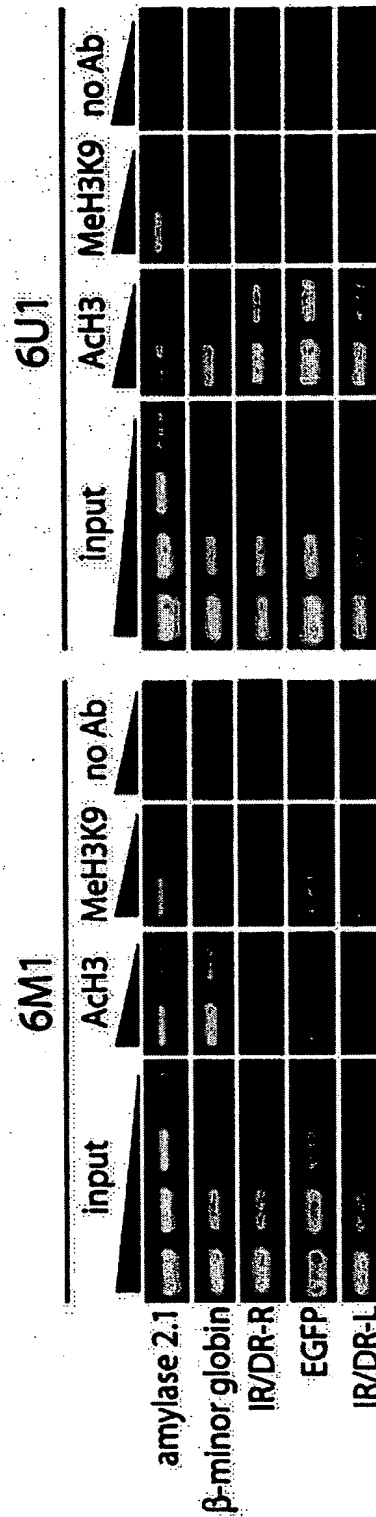


Fig. 7C



**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ BLACK BORDERS

☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

☐ FADED TEXT OR DRAWING

☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING

☐ SKEWED/SLANTED IMAGES

☒ COLOR OR BLACK AND WHITE PHOTOGRAPHS

☐ GRAY SCALE DOCUMENTS

☐ LINES OR MARKS ON ORIGINAL DOCUMENT

☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**